



GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE OF SOME PROMINENT ADVANCED LINES OF UPLAND RICE (BROADCAST AUS) GENOTYPES

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Abstract

An experiment was conducted at Plant Breeding Division, BRRI, Bangladesh during the Aus season of 2018 to study the genetic variability and inheritance of seventeen advanced lines of upland rice (*Oryza sativa* L.) by Randomized Complete Block Design (RCBD). The number of Grains per panicle showed the highest variation (70.67-123.67). The genotype G-8 showed the best performance for number of effective tiller, panicle weight, number of grain per panicle, and total spikelet per plant. In terms of early maturity (50% DF and DM), panicle length and grain yield, best performance was obtained from the genotype G-15. From the present study, effective tiller number, panicle weight, total spikelet per panicle, and grain yield showed high heritability estimates along with high genetic advance. These characters also exerted moderate to high direct effects on the grain yield. From the association study, the grain yield was found highly significant, positive, genotypic and phenotypic correlation with the effective tiller, panicle length, panicle weight, grains per panicle, total spikelet per panicle and spikelet fertility percentage. The genotypic path coefficient analysis showed that the top most significant maximum direct effect (1.6859) was found for number of grains per panicle.

Key words: Correlation; Genotypic coefficient of variation; Path analysis; Grain yield; Variance.

Introduction

Rice (*Oryza sativa*) is the most important cereal crop in Bangladesh belonging to family Poaceae (Gramineae). In Bangladesh, rice is the main source of calorie, which fulfil around eighty percent calorie demand in the form of different dietary components of the people (Kamal *et al.*, 2007). The present population growth rate predicted by 2030 need 48 million tons of extra food grain to fulfil the demand of excess population (Roy *et al.*, 2011). So it is high time to improve rice production vertically by utilizing every genetic resources judiciously.

Rice area coverage includes 13% upland ecosystem, 11% Deepwater ecosystem and 25% rainfed lowland ecosystem of the total rice area (Fukai *et al.*, 1998). Broadcast or upland rice (Aus) is in extreme emphasis for its short duration and good for accommodating more than three to four crops a year. It generally depends on rain water rather than regular irrigation scheduling. In the future context of water crisis due to climate change, upland rice ecosystem can show the vital performance in Bangladesh. Production efficiency of upland rice is less than Aman and Boro, but less water requirement and fitting ability in intensive cropping pattern of upland rice is always appreciable.

In response to the prospects of upland Aus rice, the research work has been initiated to estimate genetic variability, heritability and genetic advance of some promising genotypes. The success of high yielding variety development mostly depends on the existence of variation among pre-breeding materials (Adeyemo and Ojo, 1991). Genetic variability identification is very effective study in selection of superior parents for breeding program (Chauhan and Singh, 1982) because crop improvement depends upon degree of genetic variation among parents' population. Heritability estimate can give idea about the heritable proportion of phenotypic variance that is transfer from parents to offspring (Biswaranjan *et al.* 2017). The idea of genetic variability, heritability and genetic advance are immense help to plant breeder to formulate an effective breeding strategy (Sawant and patil 1995). Hence the present investigation was undertaken to study genetic variability among seventeen improved rice genotypes to determine agronomic traits that will be used for improving yield of the crops.

Materials and Methods

The experiment was accomplished at research field of plant breeding division, BRRI, during April 2018 to August

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2018 by Randomized Complete Block Design (RCBD) with three replications. Seventeen advanced lines of rice from upland rice development program were used in this experiment as listed in table 1. The seeds were kept in 48° C for 72 hours and soaked for a day, treated with Bavistin for 5 minutes before sowing. Seeds were sown directly in the moist field. Fertilizer rate was 60:20:40:100:10 kg/ha for N:P:K:S:Zn/ha respectively. Nitrogen was used with split application at 15, 30, 50 days after seeding (DAS). Total amount of P K Sand Zn was applied at the time of final land preparation. Herbicide was used for controlling weed population. Hand weeding was done in time. Plant protection measure was taken.

Data were recorded from five plants in each entry for each replication on plant height (cm), days to 50% flowering, days to maturity, effective tiller, panicle length, panicle weight, grains per panicle, total spikelet per panicle, spikelet fertility percentage and grain yield.

Univariate analysis of the individual character was done for all characters under study using the mean values (Islam et al., 2009) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and CV % were estimated using MSTAT-C. Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952). Broad sense heritability and expected genetic advance for different characters under selection were estimated using the formula suggested by Lush (1943). Genetic advance as percentage of mean was calculated from the following formula as proposed by Robinson et al. (1954).

Results and Discussion

The phenotypic data pertaining to ten characters have been presented and statistically analyzed with the possible explanation. The minimum and maximum values with mean value for each characters are shown in table 1. The range of variation among the genotypes in response to ten character was studied and mean sum of square, phenotypic variance (σ^2_p), genotypic variance (σ^2_g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2_b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) showed in table 1.

Table 1. Designation and mean performance of studied growth parameter and yield components of 17 upland rice genotypes

Genotypes	Designation	PH	50% DF	DM	ET	PL	PW	GP	TSP	%SF	GY
G1	BR9637-2B-2-6	82.3	75.3	100.3	7.33	22.00	1.37	70.67	83.00	85.17	3.85
G2	BR9642-2B-11-8	96.7	86.0	111.0	8.67	23.53	2.43	80.00	92.33	86.70	3.74
G3	BR9643-2B-15-13	115.7	79.7	104.7	10.33	22.43	1.87	93.00	109.33	85.09	3.70
G4	BR9722-2B-2-13	102.3	74.7	99.7	9.00	24.17	2.65	97.33	111.33	87.39	3.91
G5	BR9723-2B-3-3	111.7	76.7	101.7	10.67	24.63	2.28	97.00	106.67	90.82	3.82
G6	BR9723-2B-4-5	105.7	78.7	103.7	9.00	23.47	1.96	76.67	100.33	74.63	3.69
G7	BR9723-2B-7-8	105.3	74.0	99.0	10.67	25.10	3.15	112.67	131.33	85.81	4.52
G8	BR9101-2B-11-2-3	95.3	75.3	100.3	12.00	25.73	3.75	123.67	137.67	89.83	4.70
G9	BR9101-2B-11-2-4	88.0	74.3	99.3	8.00	24.27	2.18	97.67	108.00	90.44	3.87
G10	BR9722-2B-9-12	79.3	85.7	110.7	10.00	23.23	2.55	84.33	107.33	78.56	4.24
G11	BR9728-2B-11-3	85.0	86.7	111.7	7.00	22.57	2.35	76.00	95.33	79.79	3.64
G12	BR9728-2B-11-4	88.0	76.7	101.7	9.33	24.30	1.63	73.33	93.00	78.85	3.72
G13	BR9728-2B-1-6	78.7	87.0	112.0	8.33	22.47	1.76	81.33	96.67	84.18	4.53
G14	BR9730-2B-3-1	89.3	88.3	113.3	11.00	24.53	2.64	74.67	89.00	83.91	3.75
G15	BR9730-2B-5-4	93.0	73.7	98.7	11.67	26.80	3.49	104.67	116.67	89.76	4.86
G16	BR9642-2B-10-4	94.3	76.0	101.0	10.00	25.57	2.55	80.33	94.33	85.26	4.63
G17	BRRI dhan65	88.00	74.67	99.67	11.00	23.53	3.15	78.67	92.33	85.21	3.57
	Min	82.3	73.7	98.7	7.00	22.00	1.37	70.67	83.00	74.63	3.57
	Max	115.7	99.33	113.3	12.00	26.80	3.75	123.67	137.67	90.82	4.86
	Average	94.04	79.03	104.03	9.65	24.02	2.46	88.35	103.80	84.79	4.04

Analysis of variance (ANOVA) revealed highly significant except panicle weight and grain yield (Table 2). The phenotypic co-efficient of variation (PCV) was higher than genotypic co-efficient of variation (GCV) for all the traits thus indicated the environmental influence on these characters.

Table 2. Estimation of genetic parameters of seventeen upland rice genotypes

Traits	GenMS	Min	Max	Mean	CV (%)	σ^2_g	σ^2_e	σ^2_p	GCV	ECV	PCV	h^2_b	GA	GA (% mean)
PH	515.29**	82.3	115.7	94.04	5.52	158.52	39.72	198.24	11.02	5.52	12.33	79.97	23.19	20.31
50% DF	83.21**	73.7	99.33	79.03	0.86	27.53	0.61	28.14	5.82	0.86	5.88	97.84	10.69	11.85
DM	83.14**	98.7	113.3	104.03	0.64	27.54	0.53	28.07	4.59	0.64	4.63	98.11	10.71	9.37
ET	6.52**	7.00	12.00	9.65	6.14	2.06	0.35	2.41	14.86	6.14	16.08	85.44	2.73	28.30
PL	5.16**	22.00	26.80	24.02	0.76	1.71	0.03	1.74	5.44	0.76	5.50	98.07	2.67	11.11
PW	1.29	1.37	3.75	2.46	0.91	0.43	0.00	0.43	26.63	0.91	26.64	99.88	1.35	54.82
GP	689.31**	70.67	123.67	88.35	8.58	210.62	57.45	268.07	16.43	8.58	18.53	78.57	26.50	29.99
TSP	647.21**	83.00	137.67	103.80	6.01	202.75	38.96	241.71	13.72	6.01	14.98	83.88	26.86	25.88
%SF	62.64**	74.63	90.82	84.79	5.24	14.30	19.73	34.03	4.46	5.24	6.88	42.03	5.05	5.96
GY	0.66	3.57	4.86	4.04	0.76	0.22	0.00	0.22	11.67	0.00	11.67	100.00	0.97	24.04

* Significant at 5% level of probability ** Significant at 1% level of probability

PH- Plant height (cm), 50% DF- Days to 50% flowering, DM- Days to maturity, ET-Effective tiller, PL- Panicle length, PW-

Panicle Weight, GP- Grains per panicle, TSP- Total spikelet per panicle, %SF-Spikelet fertility percentage, GY-Grain Yield. The phenotypic variance was also higher than the genotypic variance. Wide and narrow difference between PCV and GCV for the characters implies their susceptibility and resistance to environmental fluctuation respectively. According to Prashanthi *et al.* (1990), PCV and GCV values greater than 20% are high, less than 10% are low, 10% to 20% are considered as medium. Figure 1 showed the distribution of GCV and PCV for the studied characters of the seventeen genotypes.

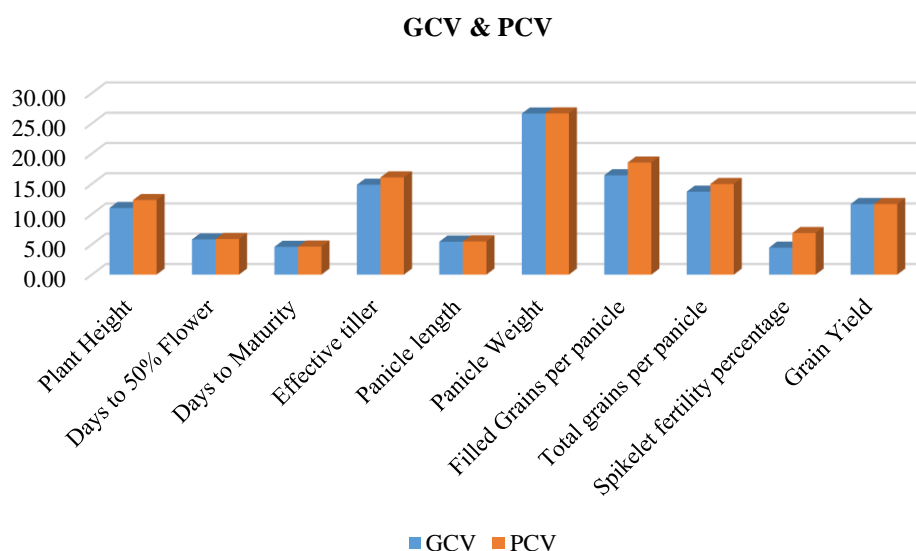


Figure 1. Distribution of GCV and PCV for the studied characters of the seventeen genotypes

The values for growth duration ranged from 98.7 to 113.3 days and least duration genotype was G-15 (Table 1). The phenotypic variance was 28.07 and genotypic variance was 27.54 respectively (Table 2). The value of PCV (4.63) and GCV (4.59) were low and difference between them was the lowest. In case of genetic variability of rice, similar findings were reported by Roy *et al.* (2011).

The lowest difference between phenotypic (5.50) and genotypic (5.44) values for co-efficient of variation indicated less influence of environment on the expression of panicle length (Table 2). Highest Panicle weight obtained from G-8 (3.75) as in table 1 and revealed negligible effect of environment as found from table 2. The PCV (26.64) was high and almost same to the GCV (26.63) for this trait. The phenotypic variance for grains per panicle (268.07) was close to genotypic variance (210.62). So, environmental impact was not considerable.

The value of PCV (18.53) and GCV (16.43) for grains per panicle was moderate and the difference was very close. Here environmental variance was high (57.45). The phenotypic variance for grains per panicle (268.07) was close to genotypic variance (210.62). This condition implies that the environmental impact on the phenotypic expression of this trait was not considerable.

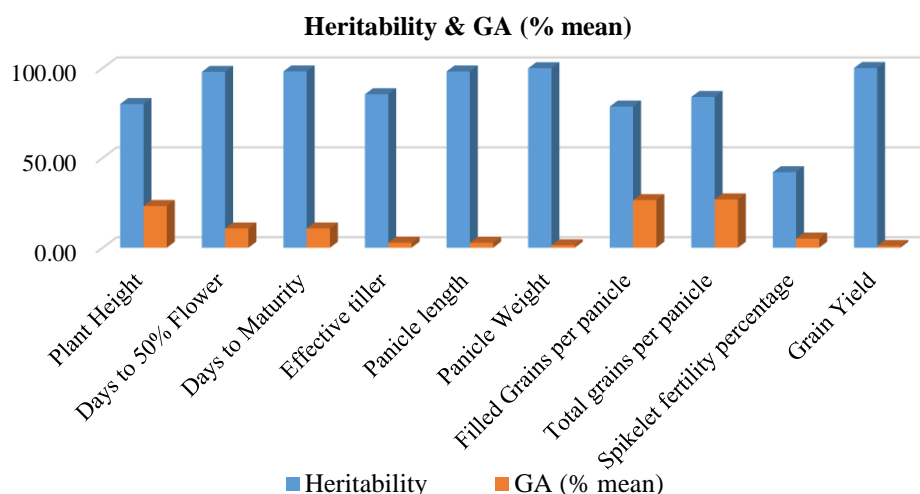


Figure 2. Heritability and genetic advance (% mean) for the studied characters of the seventeen genotypes

Total spikelet per panicle exhibited high values of GCV and PCV. The phenotypic variance for Spikelet fertility percentage (34.03) was different to genotypic variance (14.30) indicated lower influence of genotype for numbers of total spikelet per panicle. For grain yield, the highest yield obtained from G-15 (Table 1). The phenotypic variance was similar to σ_g^2 indicating that environment could not play a significant role for the expressing of the character. Heritability was 100% with high genetic advance 24.4. Selection for such trait is fruitful.

According to Kumar and Gurumurthi (2000), heritability 80% or more is very high, 40-80% is high and less than 40% is low. Here, heritability was high for 50% flowering, date of maturity, effective tiller number, panicle length, panicle weight, total spikelet per panicle, and grain yield. Heritability and genetic advance for the studied characters of the seventeen genotypes presented in figure 2.

Deshmukh *et al.* (1986) classified genetic advance as percent of mean as low (<10%), moderate (10-20%) and high (>20%). Based on this classification, plant height (cm), effective tiller, panicle weight, grains per panicle, total spikelet per panicle and grain yield had high genetic advance. Moderate genetic advance in percent of mean was computed for days to 50% flowering and panicle length. High heritability coupled with high genetic advance in percentage of mean for effective tiller number, panicle weight, total spikelet per panicle, and grain yield were obtained suggesting that these traits were highly heritable and there is a wide scope for improvement through selection of these traits. Kumari *et al.* (2007), Mahesha *et al.* (2006), Meena *et al.* (2015), Singh *et al.* (2005) and Joshi *et al.* (2004) also reported similar results. Moderately high heritability coupled with low genetic advance was obtained for spikelet fertility percentage. So, this parameter was mostly controlled by non-additive gene. This report shows the significant influence of environment and limits the scope of improvement using selection.

Association among characters

The phenotypic and genotypic correlations of yield with yield component characters are indicated in table 3. Most of the genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficient indicating the masking of the efficiency of the environment which modified the expression of a character thereby reducing the phenotypic expression (Ferrari *et al.*, 2018).

Table 3. Phenotypic and Genotypic correlation for the traits under study

		PH	50% DF	DM	ET	PL	PW	GP	TSP	%SF	GY
PH	P										
	G										
50% DF	P	-0.5710*									
	G	-0.5992*									
DM	P		0.9991**								
	G		1.0000**								
ET	P			-0.2391							
	G			-0.2488							
PL	P				-0.2363						
	G				-0.2490						
PW	P					0.6913**					
	G					0.7086**					
GP	P						0.7228**				
	G						0.7257**				
TSP	P							0.6785**			
	G							0.7086**			
%SF	P								0.9626**		
	G								0.9695**		
GY	P									0.3938	
	G									0.4043	

P for Phenotypic and G for Genotypic correlation

All the characters observed for quantitative data showed positive genotypic and phenotypic correlations with the grain yield. The grain yield had a highly significant, positive, genotypic and phenotypic correlation with the effective tiller, panicle length, panicle weight, grains per panicle, total spikelet per panicle and spikelet fertility percentage. Non-significant negative correlation was found for 50% date of flowering and for date of maturity with the grain yield (Table 3). Highly significant, positive genotypic and phenotypic correlation was also observed for 50% date of flowering with the date of maturity, effective tiller number with the panicle length and panicle weight, panicle length with panicle weight and grains per panicle, panicle weight with grains per panicle and total spikelet per panicle, grain per panicle with total spikelet per panicle and spikelet fertility percentage. Correlation coefficient for genotypic and phenotypic correlations of the traits visualized in figure 3.

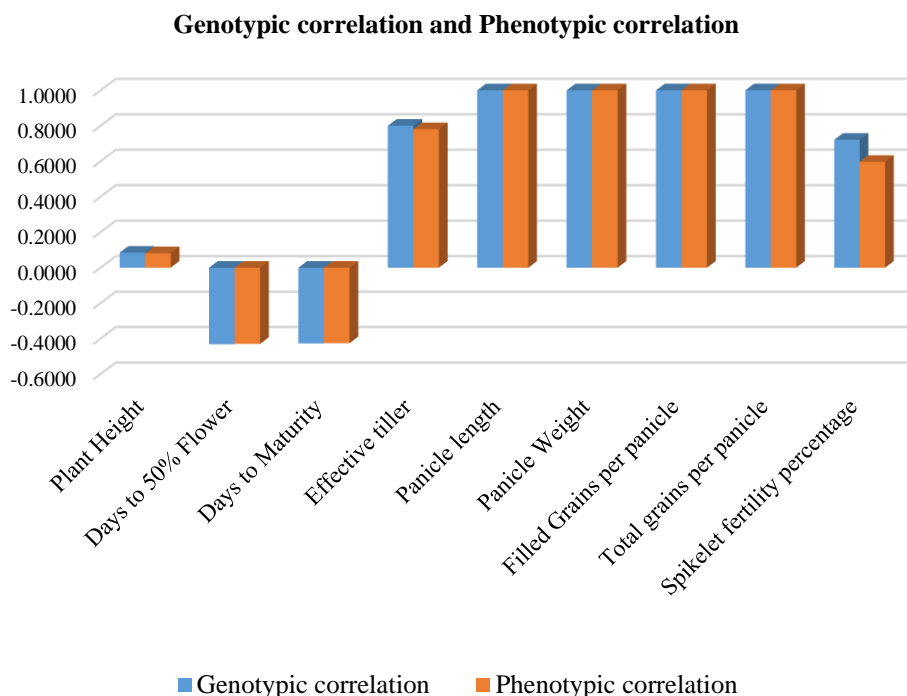


Figure 3. Correlation coefficient for genotypic and phenotypic correlations of the traits under study

Path coefficient analysis

Path coefficient analysis permits a critical examination of specific direct and indirect effects of characters.

Table 4. Path analysis showing direct (bold-diagonal) and indirect (off-diagonal) effect at genotypic level of yield component traits on grain yield of the studied rice lines

Charact ers	Indirect effect									Genotypic correlation with yield
	PH	50% DF	DM	ET	PL	PW	GP	TSP	%SF	
PH	-0.2661	-0.1629	0.0925	-0.0029	0.1316	-0.0241	0.6933**	-0.2693	-0.1074	0.0847
50% DF	0.1214	0.3156	-0.1818	-0.0098	-0.3635	0.0670	-0.8185**	0.2788	0.1592	-0.4316
DM	0.1219	0.3094	-0.1847	-0.0096	-0.3630	0.0720	-0.8016**	0.2793	0.1493	-0.4272
ET	-0.0215	-0.0211	0.0874	0.0150	0.5083*	-0.2563	0.8364**	-0.2647	-0.0832	0.8003**
PL	-0.0025	-0.1201	0.1303	0.0221	0.7377**	-0.2753	0.9289**	-0.2905	-0.1305	1.0000**
PW	0.0453	0.0011	0.0979	0.0388	0.5620*	-0.3827	1.0937**	-0.3537	-0.1023	1.0000**
GP	-0.0625	-0.1112	0.1325	0.0344	0.4254	-0.2295	1.6859**	-0.5884*	-0.2865	1.0000**
TSP	-0.0609	-0.0956	0.1247	0.0336	0.3966	-0.2261	1.6031**	-0.6233**	-0.1521	1.0000**
%SF	-0.0067	-0.0599	0.1070	0.0438	0.2884	-0.0896	1.1154**	-0.2095	-0.4676	0.7211**

Residual Effect= 0.4730238

The genotypic path coefficient analysis (Table 4) showed that the number of grains per panicle had the maximum direct effect (1.6859) followed by the panicle length (0.7377) and spikelet per panicle (0.6233). The direct effects were also highly significant. Importantly, the residual effect was 0.473 for the genotypic coefficient indicating that about 99.5 % of the genotypic total variation was contributed by the characters included in the path analysis. In case of genotypic correlation with grain yield, panicle length, panicle weight, grains per panicle and spikelet per panicle were significantly associated at 1% level of significance. The association for effective tiller and spikelet fertility percentage were also significant. Grain number per panicle showed highly significant positive indirect effect on plant height, effective tiller, panicle length, panicle weight, total spikelet per panicle and spikelet fertility (%). At the same time, highly significant negative indirect effect was observed for days to 50% flowering and days to maturity with the grain number per panicle. Thus, selection of these characters for the yield improvement is rewarding.

Conclusion

Genotype G-8 and G-15 performed better than other advanced lines for the relevant traits. So this two genotypes should be further evaluated to release as new varieties. In addition, crossing between two genotypes will generate new plants having maximum accumulation of favorable alleles, will provide the way to develop new recombinants for upland Aus rice in Bangladesh.

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